GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 16:53:39 ; Search time 156 Seconds
(without alignments)
230.757 Million cell updates/sec

Title: US-10-613-228A-1
Perfect score: 22
Sequence: 1 tcgtcgtttttcgtgcgttttt 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17.2	78.2	133	4	US-09-313-294A-108	Sequence 108, App
c	2	17.2	78.2	513	4	US-09-107-532A-292	Sequence 292, App
c	3	16.8	76.4	36016	4	US-09-949-016-14223	Sequence 14223, A
c	4	16.4	74.5	3531	1	US-08-629-600-1	Sequence 1, Appli
c	5	16.4	74.5	3531	3	US-09-076-761-1	Sequence 1, Appli
c	6	16.2	73.6	909	4	US-09-134-000C-3167	Sequence 3167, Ap
c	7	16.2	73.6	2358	4	US-09-134-000C-3285	Sequence 3285, Ap
	8	15.8	71.8	660	4	US-09-489-039A-560	Sequence 560, App
	9	15.6	70.9	231	4	US-09-543-681A-2772	Sequence 2772, Ap
c	10	15.6	70.9	300	4	US-09-543-681A-1478	Sequence 1478, Ap
	11	15.6	70.9	440	4	US-09-513-999C-35185	Sequence 35185, A
c	12	15.6	70.9	599	4	US-09-270-767-3552	Sequence 3552, Ap
c	13	15.6	70.9	599	4	US-09-270-767-18834	Sequence 18834, A
c	14	15.6	70.9	601	4	US-09-949-016-31352	Sequence 31352, A
c	15	15.6	70.9	601	4	US-09-949-016-69221	Sequence 69221, A
c	16	15.6	70.9	601	4	US-09-949-016-81370	Sequence 81370, A
c	17	15.6	70.9	601	4	US-09-949-016-127420	Sequence 127420,
c	18	15.6	70.9	601	4	US-09-949-016-177125	Sequence 177125,
c	19	15.6	70.9	601	4	US-09-949-016-177126	Sequence 177126,
c	20	15.6	70.9	601	4	US-09-949-016-177127	Sequence 177127,
c	21	15.6	70.9	678	3	US-09-134-001C-2551	Sequence 2551, Ap
	22	15.6	70.9	826	3	US-09-221-017B-1008	Sequence 1008, Ap
	23	15.6	70.9	850	3	US-08-617-860B-34	Sequence 34, Appl
c	24	15.6	70.9	1068	4	US-09-543-681A-2972	Sequence 2972, Ap
c	25	15.6	70.9	1734	4	US-09-248-796A-4704	Sequence 4704, Ap
	26	15.6	70.9	2109	4	US-09-248-796A-2999	Sequence 2999, Ap
c	27	15.6	70.9	2394	4	US-09-540-236-893	Sequence 893, App
	28	15.6	70.9	3069	3	US-08-335-865J-7	Sequence 7, Appli
c	29	15.6	70.9	3805	3	US-09-513-729B-10	Sequence 10, Appl
c	30	15.6	70.9	3805	4	US-09-023-655-1443	Sequence 1443, Ap
c	31	15.6	70.9	4071	3	US-09-513-057C-5	Sequence 5, Appli
c	32	15.6	70.9	4071	4	US-09-746-801A-5	Sequence 5, Appli
	33	15.6	70.9	4285	4	US-09-949-016-689	Sequence 689, App
	34	15.6	70.9	4308	4	US-09-394-142B-23	Sequence 23, Appl
	35	15.6	70.9	4643	2	US-08-605-106-6	Sequence 6, Appli
c	36	15.6	70.9	5061	3	US-09-355-160D-1	Sequence 1, Appli
c	37	15.6	70.9	5061	4	US-10-092-219-1	Sequence 1, Appli
	38	15.6	70.9	5296	4	US-09-949-016-2362	Sequence 2362, Ap
c	39	15.6	70.9	8302	3	US-09-234-827B-1	Sequence 1, Appli
	40	15.6	70.9	10204	4	US-09-949-016-14104	Sequence 14104, A
c	41	15.6	70.9	10482	3	US-09-322-478-23	Sequence 23, Appl
c	42	15.6	70.9	10482	4	US-09-586-106D-23	Sequence 23, Appl
	43	15.6	70.9	14066	4	US-09-601-198-56	Sequence 56, Appl
	44	15.6	70.9	26709	4	US-09-949-016-17520	Sequence 17520, A
c	45	15.6	70.9	34279	4	US-09-596-002-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-313-294A-108
; Sequence 108, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 108
; LENGTH: 133
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700548545H1
; NAME/KEY: unsure
; LOCATION: 8
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-108

Query Match 78.2%; Score 17.2; DB 4; Length 133;
Best Local Similarity 86.4%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||  ||||||  ||  |||
Db         72 TCGTCGTTGTTCGTGTGTGTTT 93
```

RESULT 2
US-09-107-532A-292/c
; Sequence 292, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA

```
;           ZIP: 02354
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: CD/ROM ISO9660
;           COMPUTER: PC
;           OPERATING SYSTEM: <Unknown>
;           SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/107,532A
;           FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 60/085,598
;           FILING DATE: 14 May 1998
;           APPLICATION NUMBER: 60/051571
;           FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Ariniello, Pamela Deneke
;           REGISTRATION NUMBER: 40,489
;           REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (781)893-5007
;           TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 292:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 513 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: circular
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;           ORGANISM: Enterococcus faecium
;       FEATURE:
;           NAME/KEY:  misc_feature
;           LOCATION: (B) LOCATION 1...513
;       SEQUENCE DESCRIPTION: SEQ ID NO: 292:
US-09-107-532A-292

  Query Match             78.2%;  Score 17.2;  DB 4;  Length 513;
  Best Local Similarity   86.4%;  Pred. No. 1.3e+02;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||| ||||||| ||||| |||
Db         76 TCGTTGTTTTTCCTGCGTCTTT 55


RESULT 3
US-09-949-016-14223/c
; Sequence 14223, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14223
;   LENGTH: 36016
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14223

  Query Match             76.4%;  Score 16.8;  DB 4;  Length 36016;
  Best Local Similarity   90.0%;  Pred. No. 2.7e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCGTTTTTCGTGCGTTTTT 22
              ||||||||| || |||||||
Db      31422 GTCGTTTTTTGTTCGTTTTT 31403


RESULT 4
US-08-629-600-1/c
; Sequence 1, Application US/08629600
; Patent No. 5783196
;  GENERAL INFORMATION:
;    APPLICANT:  NORIEGA, Fernando
;    APPLICANT:  LEVINE, Myron M.
;    TITLE OF INVENTION:  GUA MUTANTS OF SHIGELLA
;    TITLE OF INVENTION:  AND VACCINES CONTAINING THE SAME
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W., Suite 800
;      CITY:  Washington, D.C.
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/629,600
;      FILING DATE:  9-APR-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  A-6765
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3531 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-629-600-1

  Query Match             74.5%;  Score 16.4;  DB 1;  Length 3531;
  Best Local Similarity   94.4%;  Pred. No. 3.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CGTTTTTCGTGCGTTTTT 22
              |||||||||||| |||||
Db        846 CGTTTTTCGTGCATTTTT 829


RESULT 5
US-09-076-761-1/c
; Sequence 1, Application US/09076761
; Patent No. 6190669
;  GENERAL INFORMATION:
;    APPLICANT:  NORIEGA, Fernando
;    APPLICANT:  SZTEIN, Marcelo B.
;    APPLICANT:  LEVINE, Myron M.
;    TITLE OF INVENTION:  ATTENUATED MUTANTS OF SALMONELLA
;    TITLE OF INVENTION:  WHICH CONSTITUTIVELY EXPRESS THE
;    TITLE OF INVENTION:  Vi ANTIGEN
;    NUMBER OF SEQUENCES:  10
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W., Suite 800
;      CITY:  Washington, D.C.
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/076,761
;      FILING DATE:  13-MAY-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  A-7140
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3531 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-076-761-1

  Query Match             74.5%;  Score 16.4;  DB 3;  Length 3531;
  Best Local Similarity   94.4%;  Pred. No. 3.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CGTTTTTCGTGCGTTTTT 22
              ||||||||||||| |||||
Db        846 CGTTTTTCGTGCATTTTT 829


RESULT 6
US-09-134-000C-3167/c
; Sequence 3167, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3167
;   LENGTH: 909
;   TYPE: DNA
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-3167

  Query Match             73.6%;  Score 16.2;  DB 4;  Length 909;
  Best Local Similarity   85.7%;  Pred. No. 3.7e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTTT 22
              |||| |||||||||||| || |
Db        248 CGTCCTTTTTCGTGCGCTTGT 228


RESULT 7
US-09-134-000C-3285/c
; Sequence 3285, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3285
;   LENGTH: 2358
;   TYPE: DNA
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-3285

  Query Match             73.6%;  Score 16.2;  DB 4;  Length 2358;
  Best Local Similarity   85.7%;  Pred. No. 4e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTTT 22
              |||| |||||||||||| || |
Db       1697 CGTCCTTTTTCGTGCGCTTGT 1677


RESULT 8
US-09-489-039A-560
; Sequence 560, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 560
;   LENGTH: 660
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-560

  Query Match             71.8%;  Score 15.8;  DB 4;  Length 660;
  Best Local Similarity   89.5%;  Pred. No. 5.4e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCGTTTTTCGTGCGTTTT 21
              |||||||||||||  |||
Db        426 GTCGTTTTTCGTGCAGTTT 444


RESULT 9
US-09-543-681A-2772
; Sequence 2772, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
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; SEQ ID NO 2772
;   LENGTH: 231
;   TYPE: DNA
;   ORGANISM: Proteus mirabilis
US-09-543-681A-2772

  Query Match             70.9%;  Score 15.6;  DB 4;  Length 231;
  Best Local Similarity   81.8%;  Pred. No. 6.1e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              || |||||||||  || |||||
Db        167 TCCTCGTTTTTCTAGCTTTTTT 188


RESULT 10
US-09-543-681A-1478/c
; Sequence 1478, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1478
;   LENGTH: 300
;   TYPE: DNA
;   ORGANISM: Proteus mirabilis
US-09-543-681A-1478

  Query Match             70.9%;  Score 15.6;  DB 4;  Length 300;
  Best Local Similarity   81.8%;  Pred. No. 6.2e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||| ||||||  |||||| ||
Db        208 TCGTGGTTTTTTCTGCGTTGTT 187


RESULT 11
US-09-513-999C-35185
; Sequence 35185, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 35185
;   LENGTH: 440
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-35185

  Query Match             70.9%;  Score 15.6;  DB 4;  Length 440;
  Best Local Similarity   81.8%;  Pred. No. 6.4e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              | ||| |||||  |||||||||
Db        193 TTGTCCTTTTTTTTGCGTTTTT 214


RESULT 12
US-09-270-767-3552/c
; Sequence 3552, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3552
;   LENGTH: 599
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-3552

  Query Match             70.9%;  Score 15.6;  DB 4;  Length 599;
  Best Local Similarity   81.8%;  Pred. No. 6.5e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||  ||||||  |||||
Db        568 TCGTCGTGGTTCGTGTTTTTTT 547


RESULT 13
US-09-270-767-18834/c
; Sequence 18834, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18834
;   LENGTH: 599
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-18834

  Query Match             70.9%;  Score 15.6;  DB 4;  Length 599;
  Best Local Similarity   81.8%;  Pred. No. 6.5e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||  ||||||  |||||
Db        568 TCGTCGTGGTTCGTGTTTTTTT 547


RESULT 14
US-09-949-016-31352/c
; Sequence 31352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
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;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31352
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-31352

  Query Match             70.9%;  Score 15.6;  DB 4;  Length 601;
  Best Local Similarity   81.8%;  Pred. No. 6.5e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              | ||| |||||  |||||||||
Db        334 TTGTCCTTTTTTTTGCGTTTTT 313


RESULT 15
US-09-949-016-69221/c
; Sequence 69221, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69221
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-69221

  Query Match             70.9%;  Score 15.6;  DB 4;  Length 601;
  Best Local Similarity   81.8%;  Pred. No. 6.5e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              || |||||||||  | ||||||
Db        416 TCTTCGTTTTTCTGGGGTTTTT 395


Search completed: March  9, 2005, 18:48:14
Job time : 158 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 18:45:43 ; Search time 578 Seconds
(without alignments)
225.856 Million cell updates/sec

Title: US-10-613-228A-1
Perfect score: 22
Sequence: 1 tcgtcgtttttcgtgcgttttt 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	100.0	22	17	US-10-613-228A-1	Sequence 1, Appli
	2	22	100.0	22	18	US-10-816-220-152	Sequence 152, App
	3	20.4	92.7	618	18	US-10-363-345A-34257	Sequence 34257, A
c	4	20.4	92.7	618	18	US-10-363-345A-34258	Sequence 34258, A
	5	20.4	92.7	619	18	US-10-363-345A-40287	Sequence 40287, A
c	6	20.4	92.7	619	18	US-10-363-345A-40288	Sequence 40288, A
	7	20.4	92.7	761	18	US-10-363-345A-2025	Sequence 2025, Ap
c	8	20.4	92.7	761	18	US-10-363-345A-2026	Sequence 2026, Ap
	9	20.4	92.7	1024	18	US-10-363-345A-7203	Sequence 7203, Ap
c	10	20.4	92.7	1024	18	US-10-363-345A-7204	Sequence 7204, Ap
	11	19.4	88.2	511	18	US-10-363-345A-28015	Sequence 28015, A
c	12	19.4	88.2	511	18	US-10-363-345A-28016	Sequence 28016, A
	13	19.4	88.2	523	18	US-10-363-345A-35059	Sequence 35059, A
c	14	19.4	88.2	523	18	US-10-363-345A-35060	Sequence 35060, A
	15	19.4	88.2	524	18	US-10-363-345A-40325	Sequence 40325, A
c	16	19.4	88.2	524	18	US-10-363-345A-40326	Sequence 40326, A
	17	19.4	88.2	610	18	US-10-363-345A-23153	Sequence 23153, A
c	18	19.4	88.2	610	18	US-10-363-345A-23154	Sequence 23154, A
	19	19.4	88.2	838	18	US-10-363-345A-32131	Sequence 32131, A
c	20	19.4	88.2	838	18	US-10-363-345A-32132	Sequence 32132, A
	21	19.4	88.2	839	18	US-10-363-345A-1741	Sequence 1741, Ap
c	22	19.4	88.2	839	18	US-10-363-345A-1742	Sequence 1742, Ap
	23	19.4	88.2	885	18	US-10-363-345A-18089	Sequence 18089, A
c	24	19.4	88.2	885	18	US-10-363-345A-18090	Sequence 18090, A
	25	19.4	88.2	1267	18	US-10-363-345A-27261	Sequence 27261, A
c	26	19.4	88.2	1267	18	US-10-363-345A-27262	Sequence 27262, A
	27	19.4	88.2	3673778	16	US-10-312-841-2	Sequence 2, Appli
	28	19	86.4	920	18	US-10-363-345A-20285	Sequence 20285, A
c	29	19	86.4	920	18	US-10-363-345A-20286	Sequence 20286, A
	30	18.8	85.5	523	18	US-10-363-345A-17495	Sequence 17495, A
c	31	18.8	85.5	523	18	US-10-363-345A-17496	Sequence 17496, A
	32	18.8	85.5	524	18	US-10-363-345A-15599	Sequence 15599, A
c	33	18.8	85.5	524	18	US-10-363-345A-15600	Sequence 15600, A
	34	18.8	85.5	525	18	US-10-363-345A-35507	Sequence 35507, A
c	35	18.8	85.5	525	18	US-10-363-345A-35508	Sequence 35508, A
	36	18.8	85.5	553	18	US-10-363-345A-39041	Sequence 39041, A
c	37	18.8	85.5	553	18	US-10-363-345A-39042	Sequence 39042, A
	38	18.8	85.5	561	18	US-10-363-345A-35971	Sequence 35971, A
c	39	18.8	85.5	561	18	US-10-363-345A-35972	Sequence 35972, A
	40	18.8	85.5	651	18	US-10-363-345A-34913	Sequence 34913, A
c	41	18.8	85.5	651	18	US-10-363-345A-34914	Sequence 34914, A
	42	18.8	85.5	712	18	US-10-363-345A-27451	Sequence 27451, A
c	43	18.8	85.5	712	18	US-10-363-345A-27452	Sequence 27452, A
	44	18.8	85.5	759	18	US-10-363-345A-3263	Sequence 3263, Ap
c	45	18.8	85.5	759	18	US-10-363-345A-3264	Sequence 3264, Ap

ALIGNMENTS

RESULT 1
US-10-613-228A-1
; Sequence 1, Application US/10613228A
; Publication No. US20040092472A1
; GENERAL INFORMATION:
; APPLICANT: KRIEG, ARTHUR M
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS FOR STIMULATING IMMUNE RESPONES
; FILE REFERENCE: C1037.70045US00
; CURRENT APPLICATION NUMBER: US/10/613,228A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US 60/394,193
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
US-10-613-228A-1

Query Match 100.0%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||||||||||||
Db          1 TCGTCGTTTTTCGTGCGTTTTT 22
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RESULT 2
US-10-816-220-152
; Sequence 152, Application US/10816220

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; Publication No. US20040235770A1
; GENERAL INFORMATION:
;  APPLICANT: Davis, Heather L
;  APPLICANT:  McCluskie, Michael J
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID OIL-IN-WATER FORMULATIONS AND
;  TITLE OF INVENTION:  RELATED METHODS OF USE
;  FILE REFERENCE: C1037.70039US01
;  CURRENT APPLICATION NUMBER: US/10/816,220
;  CURRENT FILING DATE:  2004-04-01
;  PRIOR APPLICATION NUMBER: US 60/459,920
;  PRIOR FILING DATE: 2003-04-02
;  PRIOR APPLICATION NUMBER: US 60/461,903
;  PRIOR FILING DATE: 2003-04-10
;  NUMBER OF SEQ ID NOS: 434
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-816-220-152

  Query Match             100.0%;  Score 22;  DB 18;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||||||||||||
Db          1 TCGTCGTTTTTCGTGCGTTTTT 22


RESULT 3
US-10-363-345A-34257
; Sequence 34257, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34257
;   LENGTH: 618
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 34257
US-10-363-345A-34257

  Query Match             92.7%;  Score 20.4;  DB 18;  Length 618;
  Best Local Similarity   95.5%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||| |||||||
Db         98 TCGTCGTTTTTCGTTCGTTTTT 119


RESULT 4
US-10-363-345A-34258/c
; Sequence 34258, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34258
;   LENGTH: 618
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 34258
US-10-363-345A-34258

  Query Match             92.7%;  Score 20.4;  DB 18;  Length 618;
  Best Local Similarity   95.5%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||| |||||||
Db        521 TCGTCGTTTTTCGTTCGTTTTT 500


RESULT 5
US-10-363-345A-40287
; Sequence 40287, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40287
;   LENGTH: 619
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 40287
US-10-363-345A-40287

  Query Match             92.7%;  Score 20.4;  DB 18;  Length 619;
  Best Local Similarity   95.5%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||| |||||||
Db        190 TCGTCGTTTTTCGTTCGTTTTT 211


RESULT 6
US-10-363-345A-40288/c
; Sequence 40288, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40288
;   LENGTH: 619
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 40288
US-10-363-345A-40288

  Query Match             92.7%;  Score 20.4;  DB 18;  Length 619;
  Best Local Similarity   95.5%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||||| |||||||
Db        430 TCGTCGTTTTTCGTTCGTTTTT 409


RESULT 7
US-10-363-345A-2025
; Sequence 2025, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2025
;   LENGTH: 761
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 2025
US-10-363-345A-2025

  Query Match             92.7%;  Score 20.4;  DB 18;  Length 761;
  Best Local Similarity   95.5%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||||| |||||||
Db        598 TCGTCGTTTTTCGTTCGTTTTT 619


RESULT 8
US-10-363-345A-2026/c
; Sequence 2026, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2026
;   LENGTH: 761
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 2026
US-10-363-345A-2026

  Query Match             92.7%;  Score 20.4;  DB 18;  Length 761;
  Best Local Similarity   95.5%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||||| |||||||
Db        164 TCGTCGTTTTTCGTTCGTTTTT 143


RESULT 9
US-10-363-345A-7203
; Sequence 7203, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 7203
;   LENGTH: 1024
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 7203
US-10-363-345A-7203

  Query Match             92.7%;  Score 20.4;  DB 18;  Length 1024;
  Best Local Similarity   95.5%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||| |||||||||||||
Db        276 TCGTCGTTGTTCGTGCGTTTTT 297


RESULT 10
US-10-363-345A-7204/c
; Sequence 7204, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 7204
;   LENGTH: 1024
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 7204
US-10-363-345A-7204

  Query Match             92.7%;  Score 20.4;  DB 18;  Length 1024;
  Best Local Similarity   95.5%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||| |||||||||||||
Db        749 TCGTCGTTGTTCGTGCGTTTTT 728


RESULT 11
US-10-363-345A-28015
; Sequence 28015, Application US/10363345A
; Publication No. US20040234960A1
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; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28015
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 28015
US-10-363-345A-28015

Query Match 88.2%; Score 19.4; DB 18; Length 511;
Best Local Similarity 95.2%; Pred. No. 72;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGTCGTTTTTCGTGCGTTTTT 22
||||||||||||| ||||||||
Db 474 CGTCGTTTTTCGGGCGTTTTT 494

RESULT 12
US-10-363-345A-28016/c
; Sequence 28016, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28016
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 28016
US-10-363-345A-28016

Query Match 88.2%; Score 19.4; DB 18; Length 511;
Best Local Similarity 95.2%; Pred. No. 72;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGTCGTTTTTCGTGCGTTTTT 22
||||||||||||| ||||||||
Db 38 CGTCGTTTTTCGGGCGTTTTT 18

RESULT 13
US-10-363-345A-35059
; Sequence 35059, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35059
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 35059
US-10-363-345A-35059

Query Match 88.2%; Score 19.4; DB 18; Length 523;
Best Local Similarity 95.2%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGTCGTTTTTCGTGCGTTTTT 22
||||||||||||| ||||||||
Db 488 CGTCGTTTTTCGTTCGTTTTT 508

RESULT 14
US-10-363-345A-35060/c
; Sequence 35060, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35060
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 35060
US-10-363-345A-35060

Query Match 88.2%; Score 19.4; DB 18; Length 523;
Best Local Similarity 95.2%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGTCGTTTTTCGTGCGTTTTT 22
||||||||||||| ||||||||
Db 36 CGTCGTTTTTCGTTCGTTTTT 16

RESULT 15
US-10-363-345A-40325
; Sequence 40325, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40325
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 40325
US-10-363-345A-40325

Query Match 88.2%; Score 19.4; DB 18; Length 524;
Best Local Similarity 95.2%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 CGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||| |||||||
Db        399 CGTCGTTTTTCGTTCGTTTTT 419
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Search completed: March 9, 2005, 21:05:42
Job time : 581 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 14:14:33 ; Search time 3888 Seconds
(without alignments)
274.181 Million cell updates/sec

Title: US-10-613-228A-1
Perfect score: 22
Sequence: 1 tcgtcgtttttcgtgcgttttt 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20.4	92.7	226153	2	AC073704	AC073704 Mus muscu
	2	19.4	88.2	349980	6	AX344573	AX344573 Sequence
	3	18.8	85.5	5826	6	AX356381	AX356381 Sequence
	4	18.8	85.5	6130	6	AX251400	AX251400 Sequence
	5	18.8	85.5	6130	6	AX345031	AX345031 Sequence
	6	18.8	85.5	7728	6	AX344979	AX344979 Sequence
	7	18.8	85.5	7728	6	AX348500	AX348500 Sequence
	8	18.8	85.5	8951	6	AX345697	AX345697 Sequence
	9	18.8	85.5	13133	6	AX344227	AX344227 Sequence
	10	18.4	83.6	20	6	AX104184	AX104184 Sequence
	11	18.4	83.6	20	6	AX355698	AX355698 Sequence
	12	18.4	83.6	20	6	AX547237	AX547237 Sequence
	13	18.4	83.6	5369	6	CQ600212	CQ600212 Sequence
	14	18.4	83.6	146491	2	AC019950	AC019950 Drosophil
	15	18.4	83.6	182601	3	AC009904	AC009904 Drosophil
	16	18.4	83.6	236375	3	AE003708	AE003708 Drosophil
c	17	18.4	83.6	310967	1	AE016869	AE016869 Pseudomon
c	18	18	81.8	149269	2	BX897667	BX897667 Danio rer
c	19	17.8	80.9	1527	5	BC056691	BC056691 Danio rer
	20	17.8	80.9	2290	3	AJ606934	AJ606934 Spirula s
	21	17.8	80.9	2322	8	AY139685	AY139685 Porphyra
	22	17.8	80.9	2381	6	AX347239	AX347239 Sequence
	23	17.8	80.9	7195	6	AX277866	AX277866 Sequence
	24	17.8	80.9	7195	6	AX323551	AX323551 Sequence
	25	17.8	80.9	11622	6	AX345576	AX345576 Sequence
	26	17.8	80.9	34216	3	U57054	U57054 Caenorhabdi
	27	17.8	80.9	99176	5	BX255893	BX255893 Zebrafish
c	28	17.8	80.9	172585	2	CR847782	CR847782 Danio rer
	29	17.8	80.9	215917	2	AC006764	AC006764 Caenorhab
	30	17.8	80.9	252250	1	AP005339	AP005339 Vibrio vu
c	31	17.8	80.9	300045	1	AE016803	AE016803 Vibrio vu
c	32	17.8	80.9	303121	1	AE016766	AE016766 Escherich
	33	17.4	79.1	4110	6	AX598855	AX598855 Sequence
	34	17.4	79.1	5774	6	AX278031	AX278031 Sequence
	35	17.4	79.1	5774	6	AX323798	AX323798 Sequence
	36	17.4	79.1	5938	6	AX344811	AX344811 Sequence
	37	17.4	79.1	6067	6	AX344680	AX344680 Sequence
	38	17.4	79.1	6124	8	AB010408	AB010408 Arabidops
	39	17.4	79.1	7004	6	AX277956	AX277956 Sequence
	40	17.4	79.1	7004	6	AX323651	AX323651 Sequence
	41	17.4	79.1	7110	6	CQ806871	CQ806871 Sequence
	42	17.4	79.1	7110	6	AX251243	AX251243 Sequence
	43	17.4	79.1	7110	6	AX251990	AX251990 Sequence
	44	17.4	79.1	7110	6	AX346458	AX346458 Sequence
	45	17.4	79.1	7110	6	AX349019	AX349019 Sequence

ALIGNMENTS

RESULT 1
AC073704
LOCUS AC073704 226153 bp DNA linear HTG 29-JUN-2000
DEFINITION Mus musculus clone RP23-175I12, WORKING DRAFT SEQUENCE, 35 unordered pieces.
ACCESSION AC073704
VERSION AC073704.1 GI:8810321
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 226153)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 226153)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -------Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1804276
Center clone name: RPCI-23_175I12

Summary Statistics
Consensus quality: 200795 bases at least Q40
Consensus quality: 211634 bases at least Q30
Consensus quality: 213977 bases at least Q20
Estimated insert size: 205410; agarose-fp estimation
Estimated insert size: 222753; sum-of-contigs estimation
Quality coverage: 7.81 in Q20 bases; agarose-fp estimation
Quality coverage: 7.2 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

```
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*         1      1252: contig of 1252 bp in length
*      1253      1352: gap of unknown length
*      1353      2389: contig of 1037 bp in length
*      2390      2489: gap of unknown length
*      2490      4017: contig of 1528 bp in length
*      4018      4117: gap of unknown length
*      4118      5270: contig of 1153 bp in length
*      5271      5370: gap of unknown length
*      5371      6704: contig of 1334 bp in length
*      6705      6804: gap of unknown length
*      6805      7962: contig of 1158 bp in length
*      7963      8062: gap of unknown length
*      8063      9083: contig of 1021 bp in length
*      9084      9183: gap of unknown length
*      9184     10470: contig of 1287 bp in length
*     10471     10570: gap of unknown length
*     10571     11849: contig of 1279 bp in length
*     11850     11949: gap of unknown length
*     11950     13311: contig of 1362 bp in length
*     13312     13411: gap of unknown length
*     13412     14471: contig of 1060 bp in length
*     14472     14571: gap of unknown length
*     14572     15881: contig of 1310 bp in length
*     15882     15981: gap of unknown length
*     15982     17316: contig of 1335 bp in length
*     17317     17416: gap of unknown length
*     17417     19218: contig of 1802 bp in length
*     19219     19318: gap of unknown length
*     19319     20320: contig of 1002 bp in length
*     20321     20420: gap of unknown length
*     20421     21903: contig of 1483 bp in length
*     21904     22003: gap of unknown length
*     22004     23728: contig of 1725 bp in length
*     23729     23828: gap of unknown length
*     23829     26109: contig of 2281 bp in length
*     26110     26209: gap of unknown length
*     26210     27815: contig of 1606 bp in length
*     27816     27915: gap of unknown length
*     27916     30044: contig of 2129 bp in length
*     30045     30144: gap of unknown length
*     30145     35020: contig of 4876 bp in length
*     35021     35120: gap of unknown length
*     35121     40883: contig of 5763 bp in length
*     40884     40983: gap of unknown length
*     40984     46087: contig of 5104 bp in length
*     46088     46187: gap of unknown length
*     46188     51716: contig of 5529 bp in length
*     51717     51816: gap of unknown length
*     51817     59638: contig of 7822 bp in length
*     59639     59738: gap of unknown length
*     59739     66829: contig of 7091 bp in length
*     66830     66929: gap of unknown length
*     66930     78269: contig of 11340 bp in length
*     78270     78369: gap of unknown length
*     78370     88909: contig of 10540 bp in length
*     88910     89009: gap of unknown length
*     89010    101128: contig of 12119 bp in length
*    101129    101228: gap of unknown length
*    101229    116453: contig of 15225 bp in length
*    116454    116553: gap of unknown length
*    116554    130907: contig of 14354 bp in length
*    130908    131007: gap of unknown length
*    131008    146864: contig of 15857 bp in length
*    146865    146964: gap of unknown length
*    146965    171782: contig of 24818 bp in length
*    171783    171882: gap of unknown length
*    171883    198508: contig of 26626 bp in length
*    198509    198608: gap of unknown length
*    198609    226153: contig of 27545 bp in length.
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FEATURES             Location/Qualifiers
     source          1. .226153
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="RP23-175I12"
                     /clone_lib="RPCI mouse BAC library 23"
ORIGIN

  Query Match             92.7%;  Score 20.4;  DB 2;  Length 226153;
  Best Local Similarity   95.5%;  Pred. No. 87;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              | ||||||||||||||||||||
Db      20672 TGGTCGTTTTTCGTGCGTTTTT 20693


RESULT 2
AX344573
LOCUS       AX344573               349980 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 24 from Patent WO0200932.
ACCESSION   AX344573
VERSION     AX344573.1  GI:18492459
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of known genetic parameters within the mhc
  JOURNAL   Patent: WO 0200932-A 24 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .349980
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo
                     sapiens)~Original length of seq 1: 3.673778 <223>~split as
                     follows.~seq 01 0.000.001 TO 0.349.980~seq 02 0.300.001
                     649.980~seq 03 600.001 949.980~seq 04 900.001
                     1.249.980~seq 05 1.200.001 1.549.980~seq 06 1.500.001
                     1.849.980~seq 07 1.800.001 2.149.980~seq 08 2.100.001
                     2.449.980~seq 09 2.400.001 2.749.980~seq 10 2.700.001
                     3.049.980~seq 11 3.000.001 3.349.980~seq 12 3.300.001
                     3.649.980~seq 13 3.600.001 3.673.778 <223>~Original length
                     of seq 2: 3.673778 <223>~split as follows.~seq 14
                     0.000.001 TO 0.349.980~seq 15 0.300.001 649.980~seq 16
                     600.001 949.980~seq 17 900.001 1.249.980~seq 18 1.200.001
                     1.549.980~seq 19 1.500.001 1.849.980~seq 20 1.800.001
                     2.149.980~seq 21 2.100.001 2.449.980~seq 22 2.400.001
                     2.749.980~seq 23 2.700.001 3.049.980~seq 24 3.000.001
                     3.349.980~seq 25 3.300.001 3.649.980~seq 26 3.600.001
                     3.673.778"
ORIGIN

  Query Match             88.2%;  Score 19.4;  DB 6;  Length 349980;
  Best Local Similarity   95.2%;  Pred. No. 2.3e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTT 21
              |||||||||||| |||||||
Db     213728 TCGTCGTTTTTCGCGCGTTTT 213748


RESULT 3
AX356381
LOCUS       AX356381                5826 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 15 from Patent WO0181622.
ACCESSION   AX356381
VERSION     AX356381.1  GI:18620871
KEYWORDS    .
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with dna repair
  JOURNAL   Patent: WO 0181622-A 15 01-NOV-2001;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .5826
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 5826;
  Best Local Similarity   90.9%;  Pred. No. 6.4e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||| |||||||| ||||
Db       5567 TCGTCGTTGTTCGTGCGGTTTT 5588


RESULT 4
AX251400
LOCUS       AX251400                6130 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 368 from Patent WO0168912.
ACCESSION   AX251400
VERSION     AX251400.1  GI:15984823
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with tumor suppressor genes and
            oncogenes
  JOURNAL   Patent: WO 0168912-A 368 20-SEP-2001;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .6130
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 6130;
  Best Local Similarity   90.9%;  Pred. No. 6.4e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||| |||||||||| |||||||
Db       1332 TCGGCGTTTTTCGTTCGTTTTT 1353


RESULT 5
AX345031
LOCUS       AX345031                6130 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 102 from Patent WO0200928.
ACCESSION   AX345031
VERSION     AX345031.1  GI:18492917
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with the immune system
  JOURNAL   Patent: WO 0200928-A 102 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .6130
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 6130;
  Best Local Similarity   90.9%;  Pred. No. 6.4e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||| |||||||||| |||||||
Db       1332 TCGGCGTTTTTCGTTCGTTTTT 1353


RESULT 6
AX344979
LOCUS       AX344979                7728 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 50 from Patent WO0200928.
ACCESSION   AX344979
VERSION     AX344979.1  GI:18492865
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with the immune system
  JOURNAL   Patent: WO 0200928-A 50 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .7728
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 7728;
  Best Local Similarity   90.9%;  Pred. No. 6.3e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||||| |||| ||
Db       2026 TCGTCGTTTTTCGTTCGTTATT 2047


RESULT 7
AX348500
LOCUS       AX348500                7728 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 8 from Patent WO0202809.
ACCESSION   AX348500
VERSION     AX348500.1  GI:18614535
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of behavioural disorders, neurological disorders and
            cancer
  JOURNAL   Patent: WO 0202809-A 8 10-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .7728
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN
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  Query Match             85.5%;  Score 18.8;  DB 6;  Length 7728;
  Best Local Similarity   90.9%;  Pred. No. 6.3e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||||| |||| ||
Db       2026 TCGTCGTTTTTCGTTCGTTATT 2047


RESULT 8
AX345697
LOCUS       AX345697               8951 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 768 from Patent WO0200928.
ACCESSION   AX345697
VERSION     AX345697.1  GI:18493583
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with the immune system
  JOURNAL   Patent: WO 0200928-A 768 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .8951
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 8951;
  Best Local Similarity   90.9%;  Pred. No. 6.2e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||| |||||||||| |||||||
Db       3724 TCGGCGTTTTTCGTTCGTTTTT 3745


RESULT 9
AX344227
LOCUS       AX344227              13133 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 74 from Patent WO0200926.
ACCESSION   AX344227
VERSION     AX344227.1  GI:18492115
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with signal transduction
  JOURNAL   Patent: WO 0200926-A 74 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .13133
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 13133;
  Best Local Similarity   90.9%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||  |||||||
Db       8050 TCGTCGTTTTTCGGTCGTTTTT 8071


RESULT 10
AX104184
LOCUS       AX104184               20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 376 from Patent WO0122972.
ACCESSION   AX104184
VERSION     AX104184.1  GI:13920381
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 376 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTT 20
              |||||||||| |||||||||
Db          1 TCGTCGTTTTGCGTGCGTTT 20


RESULT 11
AX355698
LOCUS       AX355698               20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 726 from Patent WO0197843.
ACCESSION   AX355698
VERSION     AX355698.1  GI:18620366
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 726 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTT 20
              |||||||||| |||||||||
Db          1 TCGTCGTTTTGCGTGCGTTT 20


RESULT 12
AX547237
LOCUS       AX547237               20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 376 from Patent WO02053141.
ACCESSION   AX547237
VERSION     AX547237.1  GI:25812381
KEYWORDS    .
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 376 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTT 20
              ||||||||||  |||||||||
Db          1 TCGTCGTTTTGCGTGCGTTT 20


RESULT 13
CQ600212
LOCUS       CQ600212                5369 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 27970 from Patent WO0171042.
ACCESSION   CQ600212
VERSION     CQ600212.1  GI:41655454
KEYWORDS    .
SOURCE      Drosophila sp.
  ORGANISM  Drosophila sp.
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1
  AUTHORS   Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
  TITLE     Detection kits, such as nucleic acid arrays, for detecting the
            expression of 10,000 or more Drosophila genes and uses thereof
  JOURNAL   Patent: WO 0171042-A 27970 27-SEP-2001;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .5369
                     /organism="Drosophila sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:7242"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 6;  Length 5369;
  Best Local Similarity   95.0%;  Pred. No. 9.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTT 21
              ||||||||||  |||||||||
Db       3568 CGTCGTTTTTTGTGCGTTTT 3587


RESULT 14
AC019950
LOCUS       AC019950              146491 bp    DNA     linear   HTG 03-JAN-2000
DEFINITION  Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
ACCESSION   AC019950
VERSION     AC019950.1  GI:6664947
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 146491)
  AUTHORS   Adams,M. and Venter,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
            Rockville, MD, USA
COMMENT     This sequence was identified as CDM:10211502 by the submitter.
            For more information on this record e-mail to fly@celera.com.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
FEATURES             Location/Qualifiers
     source          1. .146491
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 2;  Length 146491;
  Best Local Similarity   95.0%;  Pred. No. 7.2e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTT 21
              ||||||||||  |||||||||
Db      38427 CGTCGTTTTTTGTGCGTTTT 38446


RESULT 15
AC009904
LOCUS       AC009904              182601 bp    DNA     linear   INV 06-SEP-2001
DEFINITION  Drosophila melanogaster, chromosome 3R, region 88E-88E, BAC clone
            BACR32A03, complete sequence.
ACCESSION   AC009904 AC007693
VERSION     AC009904.7  GI:15451478
KEYWORDS    HTG.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 182601)
  AUTHORS   Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
            Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
            Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
            Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
            Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
            Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
            Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
            Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
            McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
            Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
            Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
            Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,
            Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
  TITLE     Sequencing of Drosophila chromosome 3R, region 88E-88E
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 182601)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
            Rubin,G.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-SEP-1999) Drosophila Genome Center, Lawrence Berkeley
            Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT     On Sep 6, 2001 this sequence version replaced gi:13122705.
            Sequence submitted by:
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory, MS 64-121
            Berkeley, CA 94720
            This sequence was assembled using end sequences from a whole genome
```

```
           shotgun and from subclones of this BAC and its neighboring clones.
           For further information about this sequence, including its location
           and relationship to other sequences, please visit our sequence
           archive Web site (http://www.fruitfly.org/sequence/) or send email
           to bdgp@fruitfly.berkeley.edu.
FEATURES             Location/Qualifiers
     source          1. .182601
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /strain="y; cn bw sp"
                     /db_xref="taxon:7227"
                     /chromosome="3R"
                     /map="88E-88E"
                     /clone="BACR32A03 (D1083)"
                     /clone_lib="RPCI-98 (Roswell Park Cancer Institute
                     Drosophila melanogaster BAC library, partial EcoRI in
                     pBACe3.6)"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 3;  Length 182601;
  Best Local Similarity   95.0%;  Pred. No. 7e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTT 21
              |||||||||| ||||||||
Db     115651 CGTCGTTTTTTGTGCGTTTT 115670


Search completed: March  9, 2005, 18:45:34
Job time : 3894 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 17:17:45 ; Search time 3444 Seconds
(without alignments)
243.152 Million cell updates/sec

Title: US-10-613-228A-1
Perfect score: 22
Sequence: 1 tcgtcgttttttcgtgcgttttt 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20.4	92.7	433	4	BG428594	BG428594 602494726
c 2	19.4	88.2	957	9	AG126335	AG126335 Pan trogl
3	19.4	88.2	969	9	AG084147	AG084147 Pan trogl
4	19	86.4	473	7	CN197708	CN197708 TgESTzyl5
c 5	18.8	85.5	698	1	AV895065	AV895065
6	18.8	85.5	750	9	CL653482	CL653482 PRI0118c_
7	18.8	85.5	755	5	BP006348	BP006348 BP006348
8	18.8	85.5	793	9	CL659802	CL659802 PRI0135b_
c 9	18.8	85.5	1173	9	CG745933	CG745933 P039-1-A0
10	18.8	85.5	1201	3	CR704325	CR704325 Tetraodon
c 11	18.8	85.5	1372	9	CG751386	CG751386 P045-4-D0
c 12	18.4	83.6	506	2	AV955361	AV955361 AV955361
c 13	18.4	83.6	517	2	AV967757	AV967757 AV967757
c 14	18.4	83.6	651	5	BW207212	BW207212 BW207212
c 15	18.4	83.6	652	5	BW336085	BW336085 BW336085
c 16	18.4	83.6	661	5	BW362385	BW362385 BW362385
c 17	18.4	83.6	701	5	BP003979	BP003979 BP003979
c 18	18.4	83.6	706	5	BW477298	BW477298 BW477298
c 19	18.4	83.6	711	5	BW435032	BW435032 BW435032
c 20	18.4	83.6	1101	9	CNS00YYO	AL097002 Drosophil
21	18	81.8	236	7	W66251	W66251 TgESTzy92c0
c 22	17.8	80.9	246	6	CB365542	CB365542 ZF001-P00
23	17.8	80.9	285	7	CN198693	CN198693 TgESTzyl6
c 24	17.8	80.9	342	6	CB353501	CB353501 ZF001-P00
c 25	17.8	80.9	362	1	AV678562	AV678562 AV678562
c 26	17.8	80.9	374	1	AV679629	AV679629 AV679629
c 27	17.8	80.9	376	5	BW103452	BW103452 BW103452
c 28	17.8	80.9	378	1	AV894777	AV894777 AV894777
c 29	17.8	80.9	396	6	CB352916	CB352916 ZF001-P00
c 30	17.8	80.9	444	5	BW589623	BW589623 BW589623
c 31	17.8	80.9	471	1	AV679587	AV679587 AV679587
c 32	17.8	80.9	498	5	BW575333	BW575333 BW575333
c 33	17.8	80.9	498	7	CN769410	CN769410 taf32h09.
c 34	17.8	80.9	499	1	AV887894	AV887894 AV887894
c 35	17.8	80.9	504	2	AW422790	AW422790 fi47g12.y
c 36	17.8	80.9	512	4	BG892389	BG892389 fp75f08.y
37	17.8	80.9	513	7	CN769717	CN769717 taf32h09.
c 38	17.8	80.9	525	1	AV885063	AV885063 AV885063
c 39	17.8	80.9	541	4	BG307575	BG307575 fm60a07.y
c 40	17.8	80.9	544	5	BW104367	BW104367 BW104367
c 41	17.8	80.9	545	5	BW187581	BW187581 BW187581
c 42	17.8	80.9	555	5	BQ420126	BQ420126 faa14c09.
c 43	17.8	80.9	559	6	CB353813	CB353813 ZF001-P00
c 44	17.8	80.9	563	4	BI706183	BI706183 fq02d05.y
c 45	17.8	80.9	564	2	BE200845	BE200845 fk82c12.y

ALIGNMENTS

RESULT 1
BG428594/c
LOCUS BG428594 433 bp mRNA linear EST 14-MAR-2001
DEFINITION 602494726F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608342 5', mRNA sequence.
ACCESSION BG428594
VERSION BG428594.1 GI:13335100
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 433)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1350 row: d column: 07
High quality sequence stop: 132.
FEATURES Location/Qualifiers
source 1. .433
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4608342"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
ORIGIN

```
  Query Match            92.7%;  Score 20.4;  DB 4;  Length 433;
  Best Local Similarity   95.5%;  Pred. No. 1e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||| ||||||||||||||||
Db        390 TCGTCGCTTTTCGTGCGTTTTT 369


RESULT 2
AG126335/c
LOCUS       AG126335                957 bp    DNA     linear   GSS 04-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-136N20.F, genomic survey sequence.
ACCESSION   AG126335
VERSION     AG126335.1  GI:16655500
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 957)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: -21M13
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .957
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-136N20.F"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match            88.2%;  Score 19.4;  DB 9;  Length 957;
  Best Local Similarity   95.2%;  Pred. No. 2.8e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTT 21
              |||||||||||||||||| ||
Db        795 TCGTCGTTTTTCGTGCGTCTT 775


RESULT 3
AG084147
LOCUS       AG084147                969 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-081M22.F, genomic survey sequence.
ACCESSION   AG084147
VERSION     AG084147.1  GI:16635949
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 969)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: -21M13
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .969
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-081M22.F"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match            88.2%;  Score 19.4;  DB 9;  Length 969;
  Best Local Similarity   95.2%;  Pred. No. 2.8e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||| ||||||||
Db        714 CGTCGTTTTTCGGGCGTTTTT 734


RESULT 4
CN197708
LOCUS       CN197708                473 bp    mRNA    linear   EST 05-APR-2004
DEFINITION  TgESTzyl55a11.y1 TgVEG118 Tachyzoite cDNA Library-2 Toxoplasma
            gondii cDNA clone TgESTzyl55a11.y1 5', mRNA sequence.
ACCESSION   CN197708
VERSION     CN197708.1  GI:46222647
KEYWORDS    EST.
SOURCE      Toxoplasma gondii
  ORGANISM  Toxoplasma gondii
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
            Sarcocystidae; Toxoplasma.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
            Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
            Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
            Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
            Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
  TITLE     Toxoplasma EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Clifton, S.
            Toxoplasma EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: toxo@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
```

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           Seq primer: -40UP from Gibco
           High quality sequence stop: 473.
FEATURES             Location/Qualifiers
     source          1. .473
                     /organism="Toxoplasma gondii"
                     /mol_type="mRNA"
                     /strain="VEG"
                     /db_xref="taxon:5811"
                     /clone="TgESTzyl55a11.y1"
                     /dev_stage="Tachyzoite"
                     /lab_host="GC10"
                     /clone_lib="TgVEG118 Tachyzoite cDNA Library-2"
                     /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2:
                     XhoI; The library was constructed by Keliang Tang,Robert
                     Cole and L.David Sibley at Washington University. cDNAs
                     were synthesized from poly(A)+ RNAby oligo d(T) priming,
                     size-selected and directionally cloned into the Uni-ZAP XR
                     lambda vector (Stratagene). The primary library was mass
                     excised as phagemids and rescued in SOLR cells. The
                     plasmid library was recovered from the SOLR cells and
                     transformed in mass into GC10 cells forsequencing.
                     WARNING: the library may contain a small percentage
                     contaminants from human fibroblast cells."
ORIGIN

  Query Match             86.4%;  Score 19;  DB 7;  Length 473;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCGTTTTTCGTGCGTTTT 21
              |||||||||||||||||||
Db        153 GTCGTTTTTCGTGCGTTTT 171


RESULT 5
AV895065/c
LOCUS       AV895065                698 bp    mRNA    linear   EST 09-NOV-2001
DEFINITION  AV895065 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone rciad40o14 3', mRNA sequence.
ACCESSION   AV895065
VERSION     AV895065.1  GI:16884161
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rciad40o14"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 1;  Length 698;
  Best Local Similarity   90.9%;  Pred. No. 5.2e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||| ||||| |||
Db        484 TCGTCGTTTTTCATGCGTATTT 463


RESULT 6
CL653482
LOCUS       CL653482                750 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0118c_G01 - PRI0118c.B21 (750) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL653482
VERSION     CL653482.1  GI:50132352
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 750)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 9;  Length 750;
  Best Local Similarity   90.9%;  Pred. No. 5.1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              || |||||||||||| ||||||
Db        457 TCCTCGTTTTTCGTGAGTTTTT 478


RESULT 7
BP006348
LOCUS       BP006348                755 bp    mRNA    linear   EST 15-MAR-2002
DEFINITION  BP006348 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad40o14 5', mRNA sequence.
ACCESSION   BP006348
VERSION     BP006348.1  GI:19497825
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 755)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
```

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           Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
           Tel: 81-75-753-4081
           Fax: 81-75-705-1113
           Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .755
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciad40o14"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 5;  Length 755;
  Best Local Similarity   90.9%;  Pred. No. 5.1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||| ||||| |||
Db        277 TCGTCGTTTTTCATGCGTATTT 298


RESULT 8
CL659802
LOCUS       CL659802                 793 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0135b_D02 - PRI0135b.B21 (793) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL659802
VERSION     CL659802.1  GI:50144272
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 793)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .793
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 9;  Length 793;
  Best Local Similarity   90.9%;  Pred. No. 5.1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              || |||||||||||| ||||||
Db        466 TCCTCGTTTTTCGTGAGTTTTT 487

.


RESULT 9
CG745933/c
LOCUS       CG745933                 1173 bp    DNA     linear   GSS 24-OCT-2003
DEFINITION  P039-1-A09.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
            genomic survey sequence.
ACCESSION   CG745933
VERSION     CG745933.1  GI:37966859
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 1173)
  AUTHORS   Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
            Buntjer,J., van der Meulen,M. and Sommer,R.J.
  TITLE     An integrated physical and genetic map of the nematode Pristionchus
            pacificus
  JOURNAL   Mol. Genet. Genomics 269 (5), 715-722 (2003)
  MEDLINE   22835951
   PUBMED   12884007
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .1173
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Ppa EcoRI BAC Library"
                     /note="The library was generated by a partial digest of
                     the genomic DNA with EcoRI and cloning into the BAC
                     vector."
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 9;  Length 1173;
  Best Local Similarity   90.9%;  Pred. No. 5.1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              || |||||||||||| ||||||
Db        164 TCCTCGTTTTTCGTGAGTTTTT 143


RESULT 10
CR704325
LOCUS       CR704325                 1201 bp    mRNA    linear   HTC 19-AUG-2004
DEFINITION  Tetraodon nigroviridis full-length cDNA.
ACCESSION   CR704325
VERSION     CR704325.1  GI:51202234
KEYWORDS    HTC; cDNA; full-length; Tetraodon nigroviridis.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -
            : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     The sequences are based on single pass reads.
            More information available at
            http://www.genoscope.cns.fr/tetraodon.
FEATURES             Location/Qualifiers
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     source          1. .1201
                     /organism="Tetraodon nigroviridis"
                     /mol_type="mRNA"
                     /db_xref="taxon:99883"
                     /tissue_type="Eyes"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 3;  Length 1201;
  Best Local Similarity   90.9%;  Pred. No. 5.1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||||| | |||||||||
Db        558 TCGTCGTTTTCCCTGCGTTTTT 579


RESULT 11
CG751386/c
LOCUS       CG751386               1372 bp    DNA     linear   GSS 24-OCT-2003
DEFINITION  P045-4-D09.yb Ppa EcoRI BAC Library Pristionchus pacificus genomic,
            genomic survey sequence.
ACCESSION   CG751386
VERSION     CG751386.1  GI:37973790
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 1372)
  AUTHORS   Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
            Buntjer,J., van der Meulen,M. and Sommer,R.J.
  TITLE     An integrated physical and genetic map of the nematode Pristionchus
            pacificus
  JOURNAL   Mol. Genet. Genomics 269 (5), 715-722 (2003)
  MEDLINE   22835951
   PUBMED   12884007
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .1372
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Ppa EcoRI BAC Library"
                     /note="The library was generated by a partial digest of
                     the genomic DNA with EcoRI and cloning into the BAC
                     vector."
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 9;  Length 1372;
  Best Local Similarity   90.9%;  Pred. No. 5.1e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              || |||||||||||| ||||||
Db        468 TCCTCGTTTTTCGTGAGTTTTT 447


RESULT 12
AV955361/c
LOCUS       AV955361               506 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV955361 Nori Satoh unpublished cDNA library, egg Ciona
            intestinalis cDNA clone cieg08a22 5', mRNA sequence.
ACCESSION   AV955361
VERSION     AV955361.1  GI:19443660
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cieg08a22"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /clone_lib="Nori Satoh unpublished cDNA library, egg"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 2;  Length 506;
  Best Local Similarity   95.0%;  Pred. No. 7.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTT 20
              ||||||| ||||||||||||
Db        125 TCGTCGTCTTTCGTGCGTTT 106


RESULT 13
AV967757/c
LOCUS       AV967757               517 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV967757 Nori Satoh unpublished cDNA library, egg Ciona
            intestinalis cDNA clone cieg23e07 5', mRNA sequence.
ACCESSION   AV967757
VERSION     AV967757.1  GI:19457453
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cieg23e07"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /clone_lib="Nori Satoh unpublished cDNA library, egg"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 2;  Length 517;
  Best Local Similarity   95.0%;  Pred. No. 7.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy          1 TCGTCGTTTTTCGTGCGTTT 20
              ||||||| ||||||||||||
Db        117 TCGTCGTCTTTCGTGCGTTT 98


RESULT 14
BW207212/c
LOCUS       BW207212                651 bp    mRNA    linear   EST 05-NOV-2002
DEFINITION  BW207212 Nori Satoh unpublished cDNA library, cleaving embryo Ciona
            intestinalis cDNA clone cicl097a05 5', mRNA sequence.
ACCESSION   BW207212
VERSION     BW207212.1  GI:24621826
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 651)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .651
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cicl097a05"
                     /tissue_type="whole body"
                     /dev_stage="cleaving embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, cleaving
                     embryo"
ORIGIN

  Query Match             83.6%;  Score 18.4;  DB 5;  Length 651;
  Best Local Similarity   95.0%;  Pred. No. 7.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTT 20
              ||||||| ||||||||||||
Db        612 TCGTCGTCTTTCGTGCGTTT 593


RESULT 15
BW336085/c
LOCUS       BW336085                652 bp    mRNA    linear   EST 27-MAY-2004
DEFINITION  BW336085 Yutaka Satou unpublished cDNA library, embryo whole animal
            Ciona intestinalis cDNA clone ciem801o19 5', mRNA sequence.
ACCESSION   BW336085
VERSION     BW336085.1  GI:47747886
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 652)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Yutaka Satou
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4095
            Fax: 81-75-705-1113
            Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .652
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciem801o19"
                     /tissue_type="whole animal"
                     /dev_stage="embryo"
                     /clone_lib="Yutaka Satou unpublished cDNA library, embryo
                     whole animal"
ORIGIN

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Qy          1 TCGTCGTTTTTCGTGCGTTT 20
              ||||||| ||||||||||||
Db        406 TCGTCGTCTTTCGTGCGTTT 387


Search completed: March  9, 2005, 19:45:52
Job time : 3450 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 14:06:53 ; Search time 535 Seconds
(without alignments)
243.429 Million cell updates/sec

Title: US-10-613-228A-1
Perfect score: 22
Sequence: 1 tcgtcgtttttcgtgcgttttt 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	100.0	22	12	ADI16210	Adi16210 Immunosti
	2	22	100.0	22	12	ADK19243	Adk19243 Immunosti
	3	22	100.0	22	12	ADO44307	Ado44307 Nucleotid
c	4	20.4	92.7	618	6	ABQ47667	Abq47667 Oligonucl
	5	20.4	92.7	618	6	ABQ47666	Abq47666 Oligonucl
c	6	20.4	92.7	619	6	ABQ53697	Abq53697 Oligonucl
	7	20.4	92.7	619	6	ABQ53696	Abq53696 Oligonucl
c	8	20.4	92.7	761	6	ABQ15435	Abq15435 Oligonucl
	9	20.4	92.7	761	6	ABQ15434	Abq15434 Oligonucl
	10	20.4	92.7	1024	6	ABQ20612	Abq20612 Oligonucl
c	11	20.4	92.7	1024	6	ABQ20613	Abq20613 Oligonucl
c	12	19.4	88.2	511	6	ABQ41425	Abq41425 Oligonucl
	13	19.4	88.2	511	6	ABQ41424	Abq41424 Oligonucl
c	14	19.4	88.2	523	6	ABQ48469	Abq48469 Oligonucl
	15	19.4	88.2	523	6	ABQ48468	Abq48468 Oligonucl
	16	19.4	88.2	524	6	ABQ53734	Abq53734 Oligonucl
c	17	19.4	88.2	524	6	ABQ53735	Abq53735 Oligonucl
	18	19.4	88.2	610	6	ABQ36562	Abq36562 Oligonucl
c	19	19.4	88.2	610	6	ABQ36563	Abq36563 Oligonucl
	20	19.4	88.2	838	6	ABQ45540	Abq45540 Oligonucl
c	21	19.4	88.2	838	6	ABQ45541	Abq45541 Oligonucl
c	22	19.4	88.2	839	6	ABQ15151	Abq15151 Oligonucl
	23	19.4	88.2	839	6	ABQ15150	Abq15150 Oligonucl
	24	19.4	88.2	885	6	ABQ31498	Abq31498 Oligonucl
c	25	19.4	88.2	885	6	ABQ31499	Abq31499 Oligonucl
	26	19.4	88.2	1267	6	ABQ40670	Abq40670 Oligonucl
c	27	19.4	88.2	1267	6	ABQ40671	Abq40671 Oligonucl
	28	19	86.4	23	12	ADK19257	Adk19257 Immunosti
	29	19	86.4	23	12	ADK19276	Adk19276 Immunosti
c	30	19	86.4	920	6	ABQ33695	Abq33695 Oligonucl
	31	19	86.4	920	6	ABQ33694	Abq33694 Oligonucl
	32	18.8	85.5	523	6	ABQ30904	Abq30904 Oligonucl
c	33	18.8	85.5	523	6	ABQ30905	Abq30905 Oligonucl
c	34	18.8	85.5	524	6	ABQ29009	Abq29009 Oligonucl
	35	18.8	85.5	524	6	ABQ29008	Abq29008 Oligonucl
	36	18.8	85.5	525	6	ABQ48916	Abq48916 Oligonucl
c	37	18.8	85.5	525	6	ABQ48917	Abq48917 Oligonucl
	38	18.8	85.5	553	6	ABQ52450	Abq52450 Oligonucl
c	39	18.8	85.5	553	6	ABQ52451	Abq52451 Oligonucl
c	40	18.8	85.5	561	6	ABQ49381	Abq49381 Oligonucl
	41	18.8	85.5	561	6	ABQ49380	Abq49380 Oligonucl
c	42	18.8	85.5	651	6	ABQ48323	Abq48323 Oligonucl
	43	18.8	85.5	651	6	ABQ48322	Abq48322 Oligonucl
	44	18.8	85.5	712	6	ABQ40860	Abq40860 Oligonucl
c	45	18.8	85.5	712	6	ABQ40861	Abq40861 Oligonucl

ALIGNMENTS

RESULT 1
ADI16210
ID ADI16210 standard; DNA; 22 BP.
XX
AC ADI16210;
XX
DT 22-APR-2004 (first entry)
XX
DE Immunostimulatory oligodeoxynucleotide ODN 10106 SEQ ID NO:141.
XX
KW ds; immunostimulatory; antibacterial; antiallergic; antiasthmatic;
KW cytostatic; virucide; fungicide; antiparasitic; interleukin antagonist;
KW gene therapy; infectious disease; allergy; asthma; cancer.
XX
OS Unidentified.
XX
PN WO2004005476-A2.
XX
PD 15-JAN-2004.
XX
PF 03-JUL-2003; 2003WO-US021113.
XX
PR 03-JUL-2002; 2002US-0393880P.
PR 03-JUL-2002; 2002US-0394090P.
PR 03-JUL-2002; 2002US-0394091P.
PR 03-JUL-2002; 2002US-0394164P.
PR 03-JUL-2002; 2002US-0394193P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Krieg AM;
XX
DR WPI; 2004-091353/09.
XX
PT New immunostimulatory nucleic acid molecule composition comprising CpG
PT motifs, useful for diagnosing, preventing and/or treating infectious
PT diseases, allergies, asthma and cancers.
XX
PS Claim 1; SEQ ID NO 141; 257pp; English.
XX
CC The invention relates to a novel composition comprising an
CC immunostimulatory nucleic acid molecule. A composition of the invention
CC has antibacterial, antiallergic, antiasthmatic, cytostatic, virucide,

CC fungicide, and antiparasitic activity. A composition may act as an
CC interleukin antagonist-4, or interleukin antagonist-5, and may have a use
CC in gene therapy. The methods and compositions of the present invention
CC are useful for diagnosing, preventing and/or treating infectious disease,
CC allergy, asthma, cancer, where the infectious disease is a herpes simplex
CC virus, bacterial, fungal or parasitic infection, and where the cancer is
CC a biliary tract cancer, bone cancer, brain and CNS cancer, breast cancer,
CC cervical cancer, choriocarcinoma, colon cancer, connective tissue cancer,
CC endometrial cancer, oesophageal cancer, eye cancer, gastric cancer,
CC Hodgkin's lymphoma, intraepithelial neoplasms, larynx cancer, lymphomas,
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC neuroblastomas, oral cavity cancer, ovarian cancer, pancreas cancer,
CC prostate cancer, rectal cancer, sarcomas, skin cancer, testicular cancer,
CC thyroid cancer and renal cancer. The present sequence represents an
CC immunostimulatory nucleic acid molecule of the invention.
XX
SQ Sequence 22 BP; 0 A; 4 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTGCGTTTTT 22
||||||||||||||||||||||
Db 1 TCGTCGTTTTTCGTGCGTTTTT 22

RESULT 2
ADK19243
ID ADK19243 standard; DNA; 22 BP.
XX
AC ADK19243;
XX
DT 20-MAY-2004 (first entry)
XX
DE Immunostimulatory nucleic acid #289.
XX
KW immunostimulatory nucleic acid; asthma; allergy; cancer;
KW infectious disease; autoimmune disease; airway remodeling;
KW chronic obstructive pulmonary disease; asthma; IL-6; interleukin-6;
KW TNFalpha; tumour necrosis factor alpha; IFNalpha; interferon-alpha;
KW IFNgamma; interferon-gamma; IP-10; interferon inducible protein;
KW viral infection; bacteria infection; parasitic infection; ss.
XX
OS Synthetic.
XX
PN WO2004016805-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025935.
XX
PR 19-AUG-2002; 2002US-0404479P.
PR 19-AUG-2002; 2002US-0404820P.
PR 27-NOV-2002; 2002US-0429701P.
PR 14-FEB-2003; 2003US-0447377P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Samulowitz U, Vollmer J, Uhlmann E, Jurk M, Lipford G;
PI Rankin R;
XX
DR WPI; 2004-257200/24.
XX
PT New immunostimulatory nucleic acid molecule having pyrimidine-purine
PT dinucleotide and a chimeric backbone, useful in treating and preventing
PT asthma, allergy, cancer, infectious disease, autoimmune disease or airway
PT remodeling.
XX
PS Example 15; SEQ ID NO 290; 276pp; English.
XX
CC The invention relates to an immunostimulatory nucleic acid molecule
CC comprising an internal pyrimidine-purine (YZ) dinucleotide and chimeric
CC backbone, where one internal YZ dinucleotide has a phosphodiester(-like)
CC internucleotide linkage, where optionally each additional internal YZ
CC dinucleotide has a phosphodiester(-like) or stabilised internucleotide
CC linkage, where other internucleotide linkages are stabilised. The
CC oligonucleotide is useful in stimulating or modulating an immune
CC response. The medicament shifts the immune response to a Th1 biased
CC response from a Th2 biased response. The oligonucleotide is also useful
CC in the manufacture of a medicament for treating asthma, allergy, cancer,
CC infectious disease, autoimmune disease, airway remodeling or chronic
CC obstructive pulmonary disease or in treating a subject who is a smoker or
CC who is free of symptoms of asthma. The oligonucleotide is useful in
CC inducing cytokine expression, e.g. IL-6 (interleukin-6), TNFalpha (tumour
CC necrosis factor alpha), IFNalpha (interferon-alpha), IFNgamma (interferon
CC -gamma) and IP-10 (interferon inducible protein). The oligonucleotide is
CC also useful in treating and preventing infections caused by viruses,
CC bacteria and parasites. The present sequence represents an
CC immunostimulatory nucleic acid.
XX
SQ Sequence 22 BP; 0 A; 4 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTGCGTTTTT 22
||||||||||||||||||||||
Db 1 TCGTCGTTTTTCGTGCGTTTTT 22

RESULT 3
ADO44307
ID ADO44307 standard; DNA; 22 BP.
XX
AC ADO44307;
XX
DT 29-JUL-2004 (first entry)
XX
DE Nucleotide sequence of a CpG ODN of class B.
XX
KW HCV infection; CpG therapy; immunostimulatory; hepatotropic; virucide;
KW gene therapy; ss.
XX
OS Synthetic.
XX
PN WO2004039829-A2.
XX
PD 13-MAY-2004.
XX
PF 29-OCT-2003; 2003WO-IB005520.
XX
PR 29-OCT-2002; 2002US-0421987P.
XX
PA (COLE-) COLEY PHARM GROUP LTD.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Ahluwalia NK, Efler SM, Davis HL, Vollmer J;
XX
DR WPI; 2004-376156/35.
XX
PT Treating a patient having hepatitis C virus (HCV) infection that was not
PT successfully treated using a previous non-CpG therapy comprises
PT administering to a subject a CpG immunostimulatory nucleic acid.
XX
PS Example; SEQ ID NO 6; 89pp; English.
XX
CC The invention relates to treating a patient having hepatitis C virus
CC (HCV) infection that was not successfully treated using a previous non-
CC CpG therapy. The method involves administering to a subject in need of
CC such treatment a CpG immunostimulatory nucleic acid in an amount
CC effective to treat the infection. In the treatment method, the non-CpG
CC therapy includes interferon-alpha. The interferon-alpha is interferon-
CC alpha-2b, interferon-alpha-2a or consensus interferon-alpha. The non-CpG

CC therapy includes interferon-alpha or pegylated interferon-alpha and
CC ribavirin. The CpG immunostimulatory nucleic acid is A, B or C class CpG
CC immunostimulatory nucleic acid. The method further comprises
CC administering interferon-alpha to the subject. The interferon-alpha is
CC administered substantially simultaneously with the CpG immunostimulatory
CC nucleic acid. The CpG immunostimulatoy nucleic acid comprises a backbone
CC modification, preferably a phosphorothionate backbone modification. The
CC CpG immunostimulatory nucleic acid comprises a semi-soft backbone. The
CC method is useful for treating a patient having hepatitis C virus (HCV)
CC infection that was not successfully treated using a previous non-CpG
CC therapy. Sequences ADO44302-ADO44317 represent examples of CpG
CC oligodeoxynucleotides (ODN) which were used in the experiments to
CC exemplify the methods of the invention.
XX
SQ Sequence 22 BP; 0 A; 4 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTGCGTTTTT 22
||||||||||||||||||||||
Db 1 TCGTCGTTTTTCGTGCGTTTTT 22

RESULT 4
ABQ47667/c
ID ABQ47667 standard; DNA; 618 BP.
XX
AC ABQ47667;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34258.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 618 BP; 241 A; 204 C; 58 G; 115 T; 0 U; 0 Other;

Query Match 92.7%; Score 20.4; DB 6; Length 618;
Best Local Similarity 95.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTGCGTTTTT 22
||||||||||||||| |||||||
Db 521 TCGTCGTTTTTCGTTCGTTTTT 500

RESULT 5
ABQ47666
ID ABQ47666 standard; DNA; 618 BP.
XX
AC ABQ47666;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34257.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,

CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 618 BP; 115 A; 58 C; 204 G; 241 T; 0 U; 0 Other;

Query Match 92.7%; Score 20.4; DB 6; Length 618;
Best Local Similarity 95.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTGCGTTTTT 22
||||||||||||||| |||||||
Db 98 TCGTCGTTTTTCGTTCGTTTTT 119

RESULT 6
ABQ53697/c
ID ABQ53697 standard; DNA; 619 BP.
XX
AC ABQ53697;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 40288.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 619 BP; 241 A; 205 C; 57 G; 116 T; 0 U; 0 Other;

Query Match 92.7%; Score 20.4; DB 6; Length 619;
Best Local Similarity 95.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTGCGTTTTT 22
||||||||||||||| |||||||
Db 430 TCGTCGTTTTTCGTTCGTTTTT 409

RESULT 7
ABQ53696
ID ABQ53696 standard; DNA; 619 BP.
XX
AC ABQ53696;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 40287.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the

```
CC   disclosure of the invention
XX
SQ   Sequence 619 BP; 116 A; 57 C; 205 G; 241 T; 0 U; 0 Other;

  Query Match             92.7%;  Score 20.4;  DB 6;  Length 619;
  Best Local Similarity   95.5%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
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Db        190 TCGTCGTTTTTCGTTCGTTTTT 211


RESULT 8
ABQ15435/c
ID   ABQ15435 standard; DNA; 761 BP.
XX
AC   ABQ15435;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 2026.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one member,
CC   of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC   degree of hybridisation to both classes is determined from the label on
CC   the amplicon. From the ratio of labels hybridised to the two classes of
CC   oligomers, the degree of methylation is calculated. The method is used:
CC   (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 761 BP; 238 A; 332 C; 100 G; 91 T; 0 U; 0 Other;

  Query Match             92.7%;  Score 20.4;  DB 6;  Length 761;
  Best Local Similarity   95.5%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||||| |||||||
Db        164 TCGTCGTTTTTCGTTCGTTTTT 143


RESULT 9
ABQ15434
ID   ABQ15434 standard; DNA; 761 BP.
XX
AC   ABQ15434;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 2025.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one member,
CC   of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC   degree of hybridisation to both classes is determined from the label on
CC   the amplicon. From the ratio of labels hybridised to the two classes of
CC   oligomers, the degree of methylation is calculated. The method is used:
CC   (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 761 BP; 91 A; 100 C; 332 G; 238 T; 0 U; 0 Other;

  Query Match             92.7%;  Score 20.4;  DB 6;  Length 761;
  Best Local Similarity   95.5%;  Pred. No. 26;
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  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||||| |||||||
Db        598 TCGTCGTTTTTCGTTCGTTTTT 619


RESULT 10
ABQ20612
ID   ABQ20612 standard; DNA; 1024 BP.
XX
AC   ABQ20612;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 7203.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one member,
CC   of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC   degree of hybridisation to both classes is determined from the label on
CC   the amplicon. From the ratio of labels hybridised to the two classes of
CC   oligomers, the degree of methylation is calculated. The method is used:
CC   (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 1024 BP; 138 A; 122 C; 396 G; 368 T; 0 U; 0 Other;

  Query Match             92.7%;  Score 20.4;  DB 6;  Length 1024;
  Best Local Similarity   95.5%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||| ||||||||||||
Db        276 TCGTCGTTGTTCGTGCGTTTTT 297


RESULT 11
ABQ20613/c
ID   ABQ20613 standard; DNA; 1024 BP.
XX
AC   ABQ20613;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 7204.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one member,
CC   of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC   degree of hybridisation to both classes is determined from the label on
CC   the amplicon. From the ratio of labels hybridised to the two classes of
CC   oligomers, the degree of methylation is calculated. The method is used:
CC   (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 1024 BP; 368 A; 396 C; 122 G; 138 T; 0 U; 0 Other;

  Query Match             92.7%;  Score 20.4;  DB 6;  Length 1024;
  Best Local Similarity   95.5%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTTCGTGCGTTTTT 22
              |||||||| ||||||||||||
Db        749 TCGTCGTTGTTCGTGCGTTTTT 728
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RESULT 12
ABQ41425/c
ID   ABQ41425 standard; DNA; 511 BP.
XX
AC   ABQ41425;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 28016.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one member,
CC   of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC   degree of hybridisation to both classes is determined from the label on
CC   the amplicon. From the ratio of labels hybridised to the two classes of
CC   oligomers, the degree of methylation is calculated. The method is used:
CC   (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 511 BP; 180 A; 177 C; 62 G; 92 T; 0 U; 0 Other;

  Query Match             88.2%;  Score 19.4;  DB 6;  Length 511;
  Best Local Similarity   95.2%;  Pred. No. 70;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||| ||||||||
Db         38 CGTCGTTTTTCGGGCGTTTTT 18


RESULT 13
ABQ41424
ID   ABQ41424 standard; DNA; 511 BP.
XX
AC   ABQ41424;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 28015.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one member,
CC   of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC   degree of hybridisation to both classes is determined from the label on
CC   the amplicon. From the ratio of labels hybridised to the two classes of
CC   oligomers, the degree of methylation is calculated. The method is used:
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CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 511 BP; 92 A; 62 C; 177 G; 180 T; 0 U; 0 Other;

  Query Match             88.2%;  Score 19.4;  DB 6;  Length 511;
  Best Local Similarity   95.2%;  Pred. No. 70;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTTT 22
              |||||||||||| ||||||||
Db        474 CGTCGTTTTTCGGGCGTTTTT 494


RESULT 14
ABQ48469/c
ID   ABQ48469 standard; DNA; 523 BP.
XX
AC   ABQ48469;
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XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 35060.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
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CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 523 BP; 191 A; 207 C; 61 G; 64 T; 0 U; 0 Other;

  Query Match             88.2%;  Score 19.4;  DB 6;  Length 523;
  Best Local Similarity   95.2%;  Pred. No. 70;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||| |||||||
Db         36 CGTCGTTTTTCGTTCGTTTTT 16


RESULT 15
ABQ48468
ID   ABQ48468 standard; DNA; 523 BP.
XX
AC   ABQ48468;
XX
DT   12-JUL-2002  (first entry)
XX
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DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 35059.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one member,
CC   of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC   degree of hybridisation to both classes is determined from the label on
CC   the amplicon. From the ratio of labels hybridised to the two classes of
CC   oligomers, the degree of methylation is calculated. The method is used:
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CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 523 BP; 64 A; 61 C; 207 G; 191 T; 0 U; 0 Other;

  Query Match             88.2%;  Score 19.4;  DB 6;  Length 523;
  Best Local Similarity   95.2%;  Pred. No. 70;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTTCGTGCGTTTTT 22
              ||||||||||||| |||||||
Db        488 CGTCGTTTTTCGTTCGTTTTT 508


Search completed: March  9, 2005, 17:40:33
Job time : 537 secs
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